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            GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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Qy 192 TGLEGWGIKRALKQIIRSNLDIGTEHSVSTQHITSSYRDY 234	159 FAS	Qy 108 KESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIEN 158 ::: :	Query Match 5.4%; Score 127; DB 1; Length 607; Best Local Similarity 22.1%; Pred. No. 0.28; Matches 90; Conservative 63; Mismatches 147; Indels 108; Gaps 21		Brown D., Bowman S., Barrell B.G., Rajandream M.A.; Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases. This SWISS-PROT entry is copyright. It is produced through a copyright between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the EMBL between the Swiss Institute of Bioinformatics and the Bioinformatics and Bioinformatics and Bioinformatics and Bioinformatics and Bioinfo	[2] SEQUENCE OF 88-607 FROM N.A. STRAIN=S288C / AB972;			DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Hypothetical 69.8 kDa protein in RPL6A-DAK1 intergenic region.	ESC	ALIGNMENTS	42 101.5 4.3 566 I HEMAL JAMEI P03449 Influenza a 10 1.5 4.3 812 I IF38_YEAST P32497 saccharomyc 45 101.5 4.3 2748 I NUM1_YEAST Q00402 saccharomyc	0 102.5 4.3 1100 1 LM2_DOURFO 1 102.5 4.3 3106 1 LM2_DOURS 1 102 4.3 540 1 YKZ6_YEAST	7 103 4.4 566 1 HEMA_IADMS 7 103 4.4 566 1 HEMA_IADMS P£1103 103 4.4 1577 1 MYSH_ACACA P47808	4 104 4.4 550 1 HEMA_IADH2 P12583 infl 5 104 4.4 550 1 HEMA_IADH3 P12584 infl 6 103 6 4.4 3464 infl
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the European Bioinformatics Institute. They
use by non-profit institutions as long a
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01-OCT-1996
16-OCT-2001
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-!- FUNCTION: MAY PARTICIPATE IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson S.A., Wang L.L., Sparling P.F.; 
"Cloning and nucleotide sequence of frpC, 
Nelsseria meningitidis encoding a protein
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MEDLINE=94018616; Pubmed=8412674;
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Matches 80
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Hemagglutinin precursor [Contains: Hemagglu
Hemagglutinin HAZ chain].
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                                                                                                                                                                AQAAREFFKGLPSFKDLAEKFRDLFPNP--EGWID
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63; Mismatches
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Virology 131:116-127(1983).
-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITITATING INFECTION.
-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAIRMAND HA2) LINKED BY A DISULFIDE BOND.
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Influenza A virus (strain A/USSR/90/77).

Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hemagglutinin gene.";
J. Virol. 49:276-278(1984).
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                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Concannon P., Cummings I.W., Salser W.A.;
"Nucleotide sequence of the influenza virus A/USSR/90/77
hemagglutinin gene.";
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            81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ewropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
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LKYPLEAKYQPLTLPDPYQLEAAFILFKESDA------NPANSTEKFFWMRFRRGKNHS
                               ELREQLSSVSSFERFEIFPKER---SWPK-HNVTRGVTASCSHKGKSSFYRNLLWLTEKN
                                                     DMSDYLSAVS--DNF----AERICSQVPKGSNCSASVSAYMSRCAKQD-----
                                                                                                                                                                                                                                                                                                                                                                    P03437;
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PD000225; Hemagglutn; 1.
                                                                                    Similarity
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N-LINKED (GLCNAC...
A -> S (IN REF. 2).
S -> K (IN REF. 2).
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GLCNAC.
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.63;
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Envelope protein; Hemagglutinin; Glycoprotein; Signal. SIGNAL 1 16
CHAIN 17 344 HEMAGGLUTININ HA1 CHAIN.
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01-MAY-1992 (Rel. 22, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Hemagglutinin precursor [Contains: Hemagglu
                                  Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
PRIDODM; PD000225; Hemagglutn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Influenza A virus (strain A/Swine/Ukkel/1/84).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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01-MAY-1992
                                                                                          EMBL; M73775;
HSSP; P03437;
                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              J. Virol. 66:1129-1138(1992).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=92114135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hemagglutinin
                                                                                InterPro;
                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                        nonhuman hosts.
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                                                                                                                                                                                                                                         CELL RECEPTORS AND FOR INITIATING INFECTION.
SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TW
(HAL AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY
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HA2 chain].
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CARBOHYD
                                                                                                                           CIN8_YEAST P27895;
                                                                        01-AUG-1992 (Rel. 23, Created)
01-FEB-1995 (Rel. 31, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
Kinesin-like protein CINB.
CINB OR KSL2 OR YELO61C.
                                                                                                                                                 YEAST
                                                   Saccharomyces cerevisiae (Baker's Eukaryota; Fungi; Ascomycota; Sac
  SEQUENCE FROM STRAIN-S288C;
                               NCBI_TaxID-4932;
                                         Saccharomycetales;
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Query Match

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Score

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3C CRC64; Length 1038;

CONFLICT CONFLICT SEQUENCE

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> KINESIN-MOTOR (BY SIMILARITY). COILED COIL (POTENTIAL). COILED COIL (POTENTIAL). ATP (BY SIMILARITY).

Motor protein; Mitosis; Cell comain 72
DOMAIN 554

PROSITE; PS00411; PROSITE; PS50067;

Cell division; Microtubules; ATP-binding;

Coiled

coil;

KINESIN_MOTOR_DOMAIN1; 1.
KINESIN_MOTOR_DOMAIN2; 1.

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EMBL; Z11859; CAA77885.1; -.
EMBL; M90522; AA34496.1; -.
EMBL; M90522; AA365026.1; -.
EMBL; X79105; CAA55722.1; -.
PIR; B42641; B42641.
HSSP, P17119; 3KAR.
SGD; S0000787; CIN8.
InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92317149; PubMed=1618897;
Hoyt M.A., He L., Loo K.K., Saunders W.S.;
"Two Saccharomyces cerevisiae kinesin-related
for mitotic spindle assembly.";
                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saunders W.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rousselet G., Simon M., Ripoche P., Buhler J.M.; "A second nitrogen permease regulator in Saccharomyces FEBS Lett. 359:215-219(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C / AB972;
Dietrich F.S., Mulligan
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J. Cell Biol. 118:109-120(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RÉQUIRÉD FOR ASSEMBLY OF THE MITOTIC SPINDLE. INT WITH SPINDLE MICROTUBULES TO PRODUCE AN OUTWARDLY DIRECTED FORCE ACTING UPON THE POLES. FOLLOWING SPINDLE ASSEMBLY, CI KIPI APPARENTLY ACT TO OPPOSE A FORCE THAT DRAWS SEPARATED BACK TOGETHER. THIS FORCE SEEMS TO BE MEDIATE BY KAR3.
SUBCELLULAR LOCATION: SPINDLE MICROTUBULES THAT LIE BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                 European
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an email to license@isb-sib.ch).
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on M., Ripoche P
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Matches 119; Conservative
STRAIN-MC58 / SEROGROUP B;

MEDLINE-20175755; PubMed-10710307;

MEDLINE-20175755; PubMed-10710307;

Tettelln H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K. Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Melson W.C., Gwinn'M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Melson W.C., Salzberg S.L., White O., Pleischmann R.D., Dougherty B.,

Haft D.H., Salzberg S.L., White O., Fleischmann K.D., Dougherty B.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

Complete genome sequence of Neisseria meningitidis serogroup B st
                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-MC58 / SERC
                                                                                                                                                                                                          Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta su
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16-OCT-2001 (Rel. 40, Last annotation
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PROSITE; PS00330; HEMOLYSIN_CALCIUM;
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                                                   83;
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                                                                                                                                         uai protein;
                                                                                                                                                                                               IPR000087; Collagen
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Firmicutes; Bacillus/Clostridium group; Mollicutes;
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Q1-JUN-1994 (Rel. 29, Last,
Q1-JUN-1994 (Rel. 40, Last,
Q1-JUN-11, Q1-JUN-11, Last,
Q1-JUN-11, Q1-JUN-11, Q1-JUN-11, Q1-JUN-11, Q1-JUN-11, Q1-JUN-11, Q1-J
                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                          Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G., Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; "The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPL1 genes and three
                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                            Yeast
                                                                                                                                                                                                                                                                                                                 MEDLINE-93247549; PubMed-8483450;
Koelling R., Nguyen T., Chen E.Y., Bo
Koelling R., Nguyen T., Chen E.Y., Bo
"A new yeast gene with a myosin-like
Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharor
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                                        Dictyostelium discoideum Eukaryota; Mycetozoa; Dic
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L; X7341; CAA51948.1;
L; Z28320; CAA82174.1;
; S38173; S38173;
; S0001803; MLP1.
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Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
"X-ray crystal structure and solution fluorescence cha
of Mg.2'(3') O-(N-methylanthraniloy1) nucleotides boun
loctyostelium discoideum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).
-1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN
-1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN
SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT S
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS
LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT
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MEDLINE-96206189; PubMed-8611530;
Smith C.A., Rayment I.;
Smith C.A., Rayment I.;
Tray structure of the magnesium(II).ADP.vanadate
"X-ray structure of the magnesium(II).ADP.vanadate
Dictyostelium discoideum myosin motor domain to 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97452580; PubMed=9305951; Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.; "X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP of the Dictyostellum discoideum myosin motor domain."; Biochemistry 36:11619-11628(1997).
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MEDLINE=95345067; PubMed=7619796;
Smith C.A., Rayment I.;
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"X-ray structure of the magnesium(II)-pyrophosphate of truncated head of Dictyostelium discoideum myosin to
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NE=95345066; PubMed=7619795;
T.A.J., Smith C.A., Thoden J.B.,
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269:239-243(1990).
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Best Local
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DOMAIN 817 2116
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DOMAIN 638 660
DOMAIN 738 752
MOD_RES 130 130
MOD_RES 130 130
MOD_RES 1823 1823
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InterPro;
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SMART; SM00242; MYSC; 1.
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PIR; PIR; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF006512; IO; 2.
Pfam; PF00065; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
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MISCELLANGOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA A ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS A POSITION (688).

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ween the Swiss Institute of Bioinf
European Bioinformatics Institute
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S00250;
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                                                                                                             D----PYQLEAAFILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLV--FNLLEKNVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                       ALKQIIRSNL-PLDIGTEHSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLAT
                                               DAEDSQKATD
                                                                   DAD----ATDIENFASRYLYMATLYYKTYTNVD----EFGASFFNKLSFTTGLFGWGIKR
                                                                                         NNKQLPAKLEDKVVL----DQLRCNGVLEGIRITRKGFPNRIIYADFVKRYYLLAPNVPR
                                                                                                                                       SDNVVTKLENDPNIASRAKKGANFITVAAQY-----KEQLASLMATLETTNPHFVRCIIP
                                                                                                                                                             SDNFAER----ICSQVPKGSNCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLP
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                                                                                                                                                                                        91;
                                                                                                                                                                                                                                                                                                                                                                                          Coiled coil;
                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    myosin_head;
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                                                                                                                                                                                                   4.8%;
20.0%;
                                            ----AVL---KHLNIDPEQYRFG---ITKIFFRAGQLA-RIEE
                                                                                                                                                                                                                                      243871 MW;
                                                                                                                                                                                       77;
                                                                                                                                                                                                Score 113.5;
Pred. No. 10;
                                                                                                                                                                                                                                                PHOSPHORYLATION PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                       ACTIN-BINDING
ACTIN-BINDING
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                                                                                                                                                                                                                                                                        PHOSPHORYLATION
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(BY MHCK).
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X MEDLINE=97405699; PubMed=9200743;
A Ma D., Nothias F., Boyne L.J., Fischer I.;
T "Differential regulation of microtubule-associated protein 1B (M T in rat CNS and PNS during development.";
L J. Neurosci. Res. 49:319-332(1997).
C -!- FUNCTION: The function of brain MAPS is essentially unknown.
C Phosphorylated MAPIB may play a role in the cytoskeletal characteristic company neurite extension. Possibly MAPIB Binds to at two tubulin subunits in the polymer, and this bridging of sulfice might be involved in nucleating microtubules.
C stabilizing microtubules.
C stabilizing microtubules.
C stabilizing microtubules.
C with MAPIA and MAPIB proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAPB KAT
P15205; Q62958; Q9ER21; Q9QW92;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of two distinct microtubule recombinant rat MAP [B.";
                                                                                                                                                                                                                                     "Neuraxin, a novel putative structural nervous system that is immunologically associated protein 5.";
EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and sequencing of the 5' associated protein (MAPIB) encoding Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-142 FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
                                                                                                                                                                                                         DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                             TISSUE=Spinal cord;
MEDLINE=90059871; PubMed=2555150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain, and Glial tumor
                                                                                                                                                                                                                                                                                                  Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J. Stauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Bet
                                                                                                                                                                                                                                                                                                                  Rienitz A., Grenningloh G
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1541-2459 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92347374; PubMed=1639092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96257242; PubMed=8666295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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                                                                                                                                                                                                         STAGE, AND PHOSPHORYLATION
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Sciurognathi;
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thi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                         DOMAIN
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Pfam; PF00414; MAP1B_neuraxin; 10.
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                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00230; MAP1B_NEURAXIN; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nerve levels are high early in development but decrease duripostnatal development and are low in addults. In dorsal root ganglia levels remain high throughout development. INDUCTION: By nerve growth factor.

DOMAIN: Has a highly basic region with many copies of the se KKEE and KKEI//. repeated but not cortex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. There by non-profit institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules. PTM: LCl is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with both MAPIB and MAPIB. It interacts with the amino-terminal region of MAPIB (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of MAP1B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem, cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heart or muscle
                                                                                                     ESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSAYMSRCAKQDCLTL
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                                                     QSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDA----
                                                                                  ESQGSTSNSDWMKNLISPDLGVVFLNVPENLKNPEP
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THEORAELILPHGQEVDIP--
                  KNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLS
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X60370; CAC16162.1;
X16623; CAA34620.1;
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KKEE AND KKEI/V RE
LYS-RICH.
M -> V (IN REF. 1)
T -> S (IN REF. 1)
R -> K (IN REF. 3)
L -> I (IN REF. 3)
7 MW; 2E3F6872DEDB8B
                                                                                                                           76;
                                                                                                                          Score 113.5; Pred. No. 12; 76; Mismatches
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MAP1B 3.
MAP1B 5.
MAP1B 5.
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MAP1B 9.
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MEDLINE-8512006; PubMed-6098280;

Beklemishev A.B., Blinov V.M., Vasilenko S.K., Golovin S.Y.,

Gutorov V.V., Karginov V.A., Mamaev L.V., Mikryukov N.N.,

Retesov S.V., Petrenko V.A., Petrov N.A., SandakhChlev L.S.;

"Synthesis of a full-length DNA copy of the hemagglutinin gethe influenza virus A HINI subtype, its cloning and primary

structure.";
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16-OCT-2001
                                                                                                                                                                                    EMBL; M38312; AAA43171.1; -. HSSP; P03437; 5HMG.
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                                                                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                           modified and this statement
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloorg. Khim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand Influenza virus A and B group;
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SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          org. Khim. 10:1535-1543(1984).
FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE CELL RECEPTORS AND FOR INITIATING INFECTION.
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                                                                                                                                    PF00509; Hemagglutinin;
                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  requires a license agreement
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                                                                                                                              137; JHWG.
IPR001364; Hemagglutn.
Con. Hemagglutinin; 1.
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(Rel. 16, Last sequence update)
(Rel. 40, Last annotation updat
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HA2 chain].
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trand viruses; Orthomyxoviridae;
roup; Influenza A viruses;
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ProDom; PD000225; Hemagglutn; 1. Envelope protein; Hemagglutinin; SIGNAL 1 16

Glycoprotein; Signal

PRINTS; PR00329; HEMAGGLUTN12.

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Best Local S
Matches 93
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CARBOHYD
                      Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                Q104I1;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical 222.8 kDa protein C1F3.06C in chromosome
SPAC1F3.06C.
              This
                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                   STRAIN-972;
                                                                                           Schizosaccharomyces
                                                              SEQUENCE
                                                                               NCBI_TaxID=4896;
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SEQUENCE FROM N.A., MEDLINE=20532503; Powerdy L., Toda T.;
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9USQ2; Q9P954;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Spindle poole body component Alp6.
ALP6 OR SPBC902.01C OR SPBC428.20c.
                                                                                                           Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomyces.
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                                                                                         NCBI_TaxID-4896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: COMPONENT OF THE GAMMA TUBULE COMPLEX THAT IS REQUIRED FOR THE REGULATION OF BOTH INTERPHASE MICROTUBULES AND MITOTIC BIPOLAR SPINDLES.
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[2]
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SEQUENCE 832 AA; 95
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SIMILARITY: BELONGS TO THE SPB ALP6/SPC98 FAMILY.
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE FRAMESHIFT IN POSITION 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fission yeast gamma-tubulin complex is required in G(1) phase component of the spindle assembly checkpoint."; J. 19:6098-6111(2000).
                                                                                                                                                                                                     GQGTV-----DFFNKEIRDP--SKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKA
                                                                                                                                                                                                                                                                                         KLRILSSVVNDNMNQENKKRLIQVVSKYNVHGDPLIQELS---
                                                                                                                                                                                                                                                                                                                                                                                                                                    EAAFILFKESDANPANSTEKRFWMRFRR-GKNHSYFHDL-VFNLLEKNVTRDADATDIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQSSRDVSSHLL--DESISNPINIPSTEVE-----SSNFGQTRYDQVPENPQITDWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKG-----
                                                                                                                  LVKKLSYRDPHSLETVVDKAYTESINHLV--
                                                                                                                                                                          GOGDVVWKGKYFLDKELIPSFLSEELVDKIFLIGKSLNFARYGCGDFDW---
                                                                                                                                                                                                                                 ----PLYEMIENWIYK-----GELVDPYQEFF-----VKEKNGSESHD----HQ
                                                                                                                                                                                                                                                               YVDTPWY----KKWYMKLKNFMVNRVFIPTKKFFNKEIREPSKALKEKVSTDTKDLFENKI
                                                                                                                                                                                                                                                                                                                    KQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAG
                                                                                                                                                                                                                                                                                                                                                  AF INDQSLALQSLKSVISKELTNFLALIASLDSQIRADASLEKPMVTIRRCIAWTQVAKL
                                                                                                                                                                                                                                                                                                                                                                             ---NFASRYLY-MATLYYKTYTNVDEFGASFFNKLSFTTGL-----
                                                                                                                                                                                                                                                                                                                                                                                                           STEYVQFKNELALLSKRIPVQYLLQMRALSETGLLYQELKVFSNYDPSVSQSIDGDNVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGLENESSISIAHDSSRLNRSTETSSVQHTLITEADLLSSISYVLQG------I
                                                          -DFVDLLMESLGNSLDQPANTLFR
                                                                                                                                             LIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDLFENK----IGQGT
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                                                                                       KEIRDPSKALIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111.5;
                                                          542
                                                                                       446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                  YLMEEVFHLTDHLKAIKKYLLLGQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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Best Local :
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P54788;

01-OCT-1996 (Rel. 34

01-OCT-1996 (Rel. 34

01-NOV-1997 (Rel. 35

Origin recognition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gavin K.A., Hidaka M., Stillman B.;

"Conserved initiator proteins in eukaryotes.";

Science 270:1667-1691(1995).

Science 270:1667-1671(1995).

-!- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS ROLE IN BOTH CHROMOSOMAL REPLICATION AND MATHE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; ;
Saccharomycetales;
NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMO0439; BAH; 1.

DNA replication; Nuclear protein; DNA-binding; ATP-binding NP_BIND 471 478 ATP (POTENTIAL).

SEQUENCE 886 AA; 101393 MW; 2DA665EC291F182F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharor
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U40151; AAC49130.1; -. InterPro; IPR003959; AAA_subfam InterPro; IPR001025; BAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00004; AAA; 1.
Pfam; PF01426; BAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96099401; PubMed=7502077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                        449
 560
                                                                     500
                                                                                                      224
                                                                                                                                                                         167
                                                                                                                                                                                                                                              109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear SIMILARITY: BELONGS TO THE ORG SIMILARITY: SOME, TO YEAST SII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-DEPENDENT MANNER. SUBUNITS (BY SIMILARITY).
                                LLATVAGYVDTPW-YKKW--YMKLKNFMV---NRVFIPTKKFFNK-------
                                                                     FQYIEINGLKIVKASDSYEVFWQKISGEKLTSGAAMESLEFYFNKVPATKKRPIVVLLDE
                                                                                                      LQHI---
                                                                                                                                                                       ATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGT---EHSVSR
                                                                                                                                                                                                                                                                                                                  -PKGSNCSASVSAYMS---RCAKQDCLTLQSLKYPLEAKYQ-PLTLPDPYQLEAAFILFK 108
                                                                                                                                                                                                                                                                                                                                                    EAISDNESDLSEYHESKEEFANASSSDSDEEFEDYQSAEELAIVEPAKKKVRSIKPDIPI
                                                                                                                                                                                                                                                                                                                                                                                     DSVGDVTKTLLAASESVDSAANAYMINSD--MSDYLSAVSDNFAERICSQV-----
LDALVSKSQDVMYNFFNWATYSNAKLIVVAVANTLDLPERHLGNKISSRIGFTRIMFTGY
                                                                                                                                        ASIYLSLYSAI-EAGTSTSIYIAGTPGV---GKTLTVREVVK-----DLMTSADQKELPR
                                                                                                                                                                                                            HNNDLDIAALEERFRTVSAKGKMETIFSKVKKQLNSRNSKEEIVKAADFDNYLPARENEF
                                                                                                                                                                                                                                            ESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRD-ADATDIENF-ASRYLYM 166
                                                                                                                                                                                                                                                                                 SPVKSQTPLQPSAVHSSPRKFFKNNIVRAKKAYTPFSKRYKNPKDIPDLND-----IFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 34, Crearce, (Rel. 34, Last sequence update) (Rel. 35, Last annotation update) quitton complex subunit 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      4.78;
19.58;
                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110.5;
Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycotina; Saccharomycetes; cetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORC1/CDC6/CDC18 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                    DYMDTQIPALPKFAKRFSLMVVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                        198;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenylase
(EC 5.1.1.
(EC 5.1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- FUNCTION: INDUCES PEPTIDE SYNTHESIS, ACTIVATES AND INCORPORATES FIVE ANINO ACIDS, FORMS A THIAZOLINE RING BETWEEN THE FIRST TWO AMINO ACIDS AND INCOPORATES A D-GLUTAMINE IN THE FOURTH POSITION.
-I- CATALYTIC ACTIVITY: L-aspartate = D-aspartate.
-I- CATALYTIC ACTIVITY: ATP + L-phenylalanine = AMP + diphosphate + I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus licheniformis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR 2002 (Rel. 41, Last annotation update)
Bacitracin synthetase 3 (BA3) [Includes: ATP-dependent isoleucine adenylase (IleA) (Isoleucine activase); ATP-dependent D-phenylalanine adenylase (D-PheA) (D-phenylalanine activase); ATP-dependent histidine adenylase (D-PheA) (D-phenylalanine activase); ATP-dependent histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-ATCC 10716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98089193; PubMed-9427658;
Konz D., Klens A., Schoergendorfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACC_BACLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetases."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Konz D., Klens A., Schoergendorfer K., Marahiel M.A.;
"The bacitracin biosynthesis operon of Bacillus licheniformis ATCC
10716: molecular characterization of three multi-modular peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         068008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-JUL-1999
                                                            N METHYLATION (OPTIONAL).

N METHYLATION (OPTIONAL).

N MESCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC DODECAPEPTIDES, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST ABUNDANT IS BACITRACIN A, A BRANCHED CYCLIC DODECAPEPTIDE. IT CONTAINS AN N-TERMINAL LINEAR PENTAPEPTIDE MOIETY (ILE-CYS-LEU-D-GLU-ILE) WITH AN ISCLUCINE-CYSTEINE THIAZOLINE CONDENSATION PRODUCT AND A C-TERMINAL HEPTAPEPTIDE RING (LYS-D-ORN-ILE-D-PHE-HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C-TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. IT CONTAINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7,
                                                                                                                                                                                                                                                                 SUBUNIT: LARGE MULTIENZYME COMPLEX OF BA1, BA2 AND BA3.

DOMAIN: CONSISTS OF FIVE MODULES WITH TWO EPIMERIZATION DOMAINS IN THE SECOND AND FOURTH MODULES, AND A POTATIVE C-TERMINAL THIOESTERASE DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nylase (HisA) (Histidine activase); ATP-dependent D-aspartate nylase (D-aspA) (D-aspartate activase); ATP-dependent asparagine nylase (AsnA) (Asparagine activase); Aspartate racemase 5.1.1.13); Phenylalanine racemase [ATP hydrolysing]
                                                                                                                                                                                                                                                                                                                                                                                                                                                              phenylalanine.
COFACTOR: CONTAINS 5
  SIMILARITY:
                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                         ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSKKDTSGNGTGNEELQSVEIKHITKAL 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKRLKLRINPDAIEIASRKIAS-----VSGDVRRALKVVKRAVEYAENDYLKRLRYERLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THEELRTIINLRLKYLNESSFYVDPETGSSYMISPDSSTI-ETDEEEKRKDFSN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDL-----FENKI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. 4:927-937(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIR--
                                                                                                                                                                                                                                                                                                                                                                                                                            NON-RIBOSOMAL BIOSYNTHESIS
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                                                                                                                                                                                                                                                                                                                                                                                                            BACITRACIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
CONTAINS
                                      BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COVALENTLY BOUND PHOSPHOPANTETHEINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---EPSKALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDP
                                        THE
  ACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                        ATP-DEPENDENT
  CARRIER
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                                                                                                                                       Envelope protein;
                                                                                                                                                       Pfam; PF00509; Hemagglutinin; PRINTS; PR00329; HEMAGGLUTN12. ProDom; PD000225; Hemagglutn;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caton A.J., Brownlee G.G., Yewdell J.W., (
"The antigenic structure of the influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR A CELL RECEPTORS AND FOR INITIATING INFECTION.
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; P03437; 5HMG
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IPRO01364; Hemagglutn.
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HEMAGGLUTININ HA1 CHAIN.
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Influenza A viruses;
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O1-NOV-1995 (Rel. 32, Created)
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30-MAY-2000 (Rel. 39, Last annotation
Nuclear fusion protein tht1.
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THT1 OR SPAC13C5.03.
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MEDLINE-98106170; PubMed=9442101;

MEDLINE-98106170; PubMed=9442101;

Tange Y., Horio T., Shimanuki M., Ding

Tange Y., Horio T., Shimanuki M., Ding

Tange Y., Horio T., Shimanuki M., Ding

Tange Y., Indiana M., In
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VARIANT
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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TRANSMEM 434 454
CARBOHYD 163 163
CARBOHYD 372 372
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    Hypothetical
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Z50112; CAA90454.1;
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(Rel. 33, Created)
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1 lipoprotein MG338 precursor.
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Best Local Similarity
Matches 114; Conserv
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LIPID
SEQUENCE
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MEDLINE-96026346; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete
SIGNAL
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STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.N., Hu p.-C., Bott K.F., Hut
"A survey of the Mycoplasma genitalium
sequencing.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma genitalium.
Bacteria; Firmicutes;
Mycoplasmataceae; Myco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Lipoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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                                                                                                                     FNLLEKNYTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASF--
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                                                                                                                                                    SPNKRNFEKQAEVLLMRFLQGQTNNFSKDNVSFSVDLFGSNSEFRSWANRNTTLKLYTAL
                                                                                                                                                                                                              FDAVRMESNSSQAQVVTSNLLVSLSSKTTQKQQQKPVYVRGDDAIYAFHIDGGNYFLENS
                                KLNNFRTDLANIEKLEQAIVDRANNYIKLQKEAKESSIGWGQPLPYKRANDGSYPSLAKF
                                                                                         TTMLENGTSNNNGQKDVCDLAKKLLKNNTNLSETIKKQQDFNNSLSQIKSSYESYIKAAN
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17.78;
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HYPOTHETICAL LIPOPROTEIN MG338.
N-ACYL DIGLYCERIDE (POTENTIAL).
W; FCE6042067310A70 CRC64;
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by using
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L: M18835; AAA43172..
SP; P03437; 2HMG.
InterPro; IPR001364; Hemagglu.,
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutinin; 1.
velope protein; Hemagglutinin; Gl.
17 344 HEM
346 566 HF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HAZ chain].
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-86186951; PubMed-3964310;
Beklemishev A.B., Blinov V.M., Va.
Karginov V.A., Mamayev L.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain A/Kiev/59/79).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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Influenza A virus
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REDLINE=96337999; PubMed=8688087;

RX MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D.,

RA Scutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

The Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

PAN Cotton M.D., Roberts K.M., Smith H.O., Woese C.R., Venter J.C.;
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Q58547;
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                                                                                                                                                                                                      Methanococcus
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Best Local S
Matches 44
                                                              VITOLOGY 162:160-166(1988).

VITOLOGY 162:160-166(1988).

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VICELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HA1 AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88101364; PubMed-3336940;
Kida H., Shortridge K.F., Webster
"Origin of the hemagglutinin gene
                                                                                                                                                                                                                                                Influenza virus A Influenza A virus. NCBI_TaxID=11498;
                                                                                                                                                                                                                                                                                                                                                 HEMA_IAZH3 STANDARD; PRT; 550 AA.

P11134; Q84025; Q84026;
O1-JUL-1989 (Rel. 11, Created)
O1-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin [Contains: Hemagglutinin HA1 chain; Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  the
                                                                                                                                                                                                                                                                            Influenza A virus (strain A/Swine/Hong Kong/126/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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N-LINKED (GLCNAC.
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Last sequence update)
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HEMA_IADH6 STANDARD; PRT; 550 AA. P12587; Q84017; P12587; Q84017; O1-OCT-1989 (Rel. 12, Created) O1-APR-1990 (Rel. 14, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hemagglutinin precursor [Contains: Hemagglutinin]
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
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-!- CATALYTIC ACTIVITY: N nucleos
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=87265458; PubMed=2440178; Kida H., Kawaoka Y., Naeve C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL RECEPTORS AND FOR INITIATING INFECTION.
-:- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO
-(HAI AND HA2) LINKED BY A DISULFIDE BOND.
-:- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Envelope protein; Hemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00509; Hemagglutinin; ProDom; PD000225; Hemagglutn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M16742; AAA43148.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 159:109-119(1987)
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Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Duck/Hokkaido/9/85).
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InterPro; IPR001364; Hemagglutn
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                                                                                                                                                                                                                                                                                                                                                                    Local
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AIAGFIENGWEGMIDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFH
                                                                                                                   VLVINSNGN--LIAPRGYFKMRT----GKS----
                                                                                                                                                                            TNLYVQASGGVTVSTRRSQQTIIPNIGSRPWVRGQSGRISIYW-----TVVKPGD
                                                                                                                                                                                                        --LFKESDANPANSTEK-------RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDAD
                                                                                                                                                                                                                                                                                              ERSNAFSNCYPY--DVPDYASLRSLVASSGTLEFITEGFTWTGVTQNGGSNACKRGPN--
                                                                                                                                                                                                                                                                                                                          ESVDSAANAYMINSDMSDYLS--------AVSDNFAERICSQVPKGS
                                                                                      LDIGTEHSVSRLQHITSS--YKDYMDTQIPALPKFAKRFSLMV----
                                                                                                                                                ATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLP
                                                                                                                                                                                                                                                                 NCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFI-------
                                                          IDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQTRGLFG
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                     SGFFSRL----NWLTKSGSTYPV----LNVTMPNNDNFDKLYIWGVHHPSTNQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                  550 AA;
                                                                                                                                                                                                                                                                                                                                                         Conservative
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550
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285
483
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                                                                                                                                                                                                                                                                                                                                                                                                                             HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. . ) (POTE
                                                                                                                                                                                                                                                                                                                                                                     Score 106;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                  67BCD85F44736CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Webster
                           --MKLK-----NEMVNRVFIPTKKEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oster R.G.;
of H3 influenza
                                                                                                                                                                                                                                                                                                                                                                     DB 1;
.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                      -----VQRLLA
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                                                                                                                   -SIMRSDAP
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HEMA_IADH7
IID HEMA_I
ACC PL2588
DT 01-OCT
DT 01-OCT
DT 16-OCT
CC Influe
OC Influe
OC Influe
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) HBMA_IADH7
) HBMA_IADH7
) HBMA_IADH7
2 P1258B; 084018; 089470;
C P125BB; 084018; 089470;
T 01-0CT-1989 (Rel. 12, Created)
T 01-0CT-1989 (Rel. 12, Last sequence update)
DT 16-0CT-2001 (Rel. 40, Last annotation update)
DE Hemagglutinin precursor [Contains: Hemagglutinin HA]
DE Hemagglutinin HA2 chain] (Fragment).
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                                                                 Query Match
Best Local S
Matches 92
                                                                                                                                    CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                           InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutn; 1. Envelope protein; Hemagglutinin; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-87265458; PubMed-2440178; Kida H., Kawaoka Y., Naeve C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 159:109-119(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Antigenic and genetic conservation ducks.";
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M16743; AAA43149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza virus A and Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11363;
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                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR AT CELL RECEPTORS AND FOR INITIATING INFECTION. SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
ERSNAFSNCYPY -- DVPDYASLRSLVASSGTLEFITEGFTWTGVTQNGGSNACKRGPN--
                                                                                                                                                                                                                                                                                                                                                                              G27813;
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                               ESVDSAANAYMINSDMSDYLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HA1 AND HA2) LINKED BY A DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KIYHKCDNVCIESIRNGTYD 487
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                                                                 92; Conservative
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                                                               Score 106; DB Pred. No. 5.9; S5; Mismatches
                                                                                                                                                                                    N-LINKED
N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                       HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
                                                                                                                                    6EF81793281D53EB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H3 influenza virus
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                                 ----AVSDNFAERICSQVPKGS
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                                                                                                 Length
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(POTENTIAL).
(POTENTIAL).
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YM08_YEAST
            EMBL; Z49702;
EMBL; Z49273;
SGD; S0004725
Hypothetical
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                 Submitted [2]
                                                                                                                                                                                the
                                                                                                                                                                                                               This
                                                                                                                                                                                                                                             Hunt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 71.4 kDa protein in ILVZ-ADE17 1
YMR119W OR YM9718.18 OR YM8564.01.
                                                                                                              or send
                                                                                                                                               modified
                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 345-624 FROM N.A. STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-431 FROM N.A. STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YM08_YEAST
P54074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales;
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35; 249702; CAA89957.1; -.
3L; 249702; CAA89268.1; -.
3L; 249273; CAA89268.1; -.
5; S0004725; YMR119W.
5; S0004725; YMR119W.
5; POTENTIAL.
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                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                  s.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LFKESDANPANSTEK------RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRKVYTEADDLFENKIGQGTVD 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDIGTEHSVSRLQHITSS--YKDYMDTQIPALPKFAKRFSLMV-----
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                                                                                                                an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KEIREPSKALK--EKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKD
                                                                                                             non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Bowman S., I
d (MAY-1995)
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                                                                    the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin that the chain] (Fragment).
                                                                                                                                                                                                                                                         WEDLINE=91391491; runner across to kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
"Molecular evidence for a role of domestic ducks in the molecular evidence for a role of domestic ducks in the molecular evidence for a role of domestic ducks in the
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=91341491; Pubmed=1875195;
                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (strain A/Duck/Hong Kong/7/75).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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                                     EMBL; D00929; HSSP; P03437;
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                                                                                                                                                                                    SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                       SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                 SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Hemagglutinin precursor [Contains: Hemagglu
                                                          Viruses; ssRNA negative-strand viruses; Orthomyxovi Influenza virus A and B group; Influenza A viruses; Influenza A viruses; Influenza A virus.
NCBI_TaxID=11378;
                        SEQUENCE FROM N.A. MEDLINE-83110955;
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 Hauptmann R., Clarke
"Nucleotide sequence
                                                                                              Influenza A virus (strain A/England/321/77).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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Mountford R.C., e haemagglutinin
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Pred. No. 6.4;
59; Mismatches
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J. Gen. vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.

SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAILBRITH AND HAZ) LINKED BY A DISULFIDE BOND.
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European Bioinformatics Institute. There are no restrictions on
 LIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDLFENKIGQGTVD
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                                                DLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKA
                                                                         EGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKI
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Pred. No. 6.6;
73; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Hypothetical
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01-NOV-1997
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                         LNLLKELSIPELNSSLGLVDVLFDGITDSDGLYERL-
                                                                                                  ALK--EKVSNDAKDLFENKIGOGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGOGTV 395
                                                                                                                             KNLVGKGKYLNTHVK--AEDVKKDVNANIKNQFDIAKIIAELMGKALKEFGNQQEGQPLS
                                                                                                                                                       RVFIPTKKFFNKEIREPSKALKEKVSTDTKDLFE-----NKIGQGTVDFFNKEIRDPSK
                                                                                                                                                                                 SLPDYTLGLNYMFDHITLNGKVVNKFSFNPFKTNLNLA-----FSNYYNGVDVFEAQ
                                                                                                                                                                                                         SYKD----YMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVN
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(Rel. 35, Last sequence up
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1 protein MG075 homolog (GC
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PubMed-8948633;
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Pred. No. 14
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Best Local Similarity
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative translational activator C18G6.05C (GSPAC18G6.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAQ5_SCI
Q10105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Connor R., Churcher C.M., Barrell B.G., Rajand Submitted (DEC-1995) to the EMBL/GenBank/DDBJ-1-SIMILARITY: STRONG, TO YEAST GCN1.
-:- SIMILARITY: CONTAINS 19 HEAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
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                                         342 TFKDLSANASDNESLSRVASELITSLRTGKVTASDQRVLFVDALSSLSLKHIDASMLLNE
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TLPDPYQLEAAFILFKESDANP-ANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDA 151
                                                                                VPKGSNCSASVSAYMSRCAKQ-----
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Best Local
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01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 94.0 kDa protein in POL-LEF3 intergenic region.
Autographa californica nuclear polyhedrosis virus (ACMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                         polyhedrosis virus.";
Virology 202:586-605(1994).
-!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94303173; PubMed=8030224; Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D. "The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P41467;
                                                                                                                                                                                         Hypothetical protein.
DOMAIN 106 117
                                                                                                                                                                                                                        EMBL; L22858; AAA66696.1;
                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                               SENVRKIKQLERSNKELNDTVQKLRDENAERLSEIQLQKG-----DLDEYKNMNRQLNED
                                                                            SESVDSAANAYMINSDMSDYLSAVSDNFAERICS-QVPKGSNCSASVSAY--MSRCAKQD
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99; Conser
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                                                                                                                                                                          93973 MW;
                                                                                                                          4.5%;
                                                                                                             ; 88
                                                                                                          Score 105; DB
Pred. No. 11;
88; Mismatches
                                                                                                                                                                        POLY-PRO.
76A871D2B6633F8A CRC64;
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                                                                                                                                         DB 1;
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01-APR-1990 (Rel. 14, L
16-OCT-2001 (Rel. 40, L
Neurofilament triplet M
(Neurofilament medium p
                                                                                                                                                                                                      SEQUENCE OF 259-857 FROM N.A.
MEDLINE=88112814; PubMed=3123320;
Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.;
"Identification of gene products expressed in the developing
visual system: characterization of a middle-molecular-weight
neurofilament CDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutearchosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                 ZOPf D., Dineva B., Betz H., Gundelfinger E.D.;
"Isolation of the chicken middle-molecular weight neurofilament
(NF-M) gene and characterization of its promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFM_CHICK P16053;
                                                                                                                                                                                                                                                                                                                         Nucleic
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90174973;
Zopf D., Dineva B
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
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                                                                                 es Dev. 1:699-708(1987).
es Dev. 1:699-708(1987).
FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINGS IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE MAINTENANCE
           PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTOF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
 SIMILARITY:
                                                                              OF AXONAL CALIBER
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 BELONGS
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                                                                                                                                                                                                                                                                                                                                                                    PubMed=2106668;
., Betz H., Gund
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t M protein (160 kDa r
um polypeptide) (NF-M)
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EMBL; X05558; CAA29073.1; -
PIR; A27040; A27040.
PIR; S08061; S08061.
PIR; S15762; S15762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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INIT_MET
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L-----FENKIGQGTVDFINKEIRDPSKALIRKVSTEA
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                                    VKMALDIEIAAYRKLLEGEETRFSAFSGSITGPIFTH---RQPSVTIASTKIQKTKIEPPK
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                                                                                  SLERQLSD
                                                                                                        FFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIR----
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                                                                                                                                                       KKWYMKLKNEMVNRVFIPTKKEENKEIREPSKALKEKVSTDTKDLFENKIG---
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COIL 1A.

LINKER 1.

COIL 1B.

LINKER 12.

COIL 2A.

LINKER 2.

COIL 2B.

O-LINKED (GLCNAC) (BY S.

O-LINKED (GLCNAC) (BY S.

G -> R (IN REF. 2).

My: 4EZEOFC6AC64778B CRC6.
                                                                                                                                 -EQNKEAIRSAKEEIAEYRRQLQSKSIELESVRGTKE
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Pred. No. 12;
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Q58900;
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Pfam;
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STRAIN-BLL-1 / DSM 2661 / ATCC 43067:

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Keiley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
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16-OCT-2001
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                                                                                                                                                                                                       Pfam; PF00271; helicase_C; 1.
Pfam; PF00063; HHH; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                  TIGR; MJ1505; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                    SEQUENCE
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                       DSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASVS
 NSIADVTKTELIE----
                                                                                                                                                                                           SM00278; HhH1; 1.
                                                              Similarity
                                                                                                                                                                               PS00690; DEAH_ATP_HELICASE; FALSE_NEG.
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IPR001650;
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                                                                                                    MΨ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the methanogenic archaeon, Methanococcus
                                                  91;
                                                Score 104.5;
Pred. No. 11;
91; Mismatches
                                                                                                               ATP (POTENTIAL)
DEAH BOX.
POLY-GLU.
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=87265458; PubMed=2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.
                                                                                                                                                                          -I-FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING CELL RECEPTORS AND FOR INITIATING INFECTION.
-I-SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED E (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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SEQUENCE
                                                                  HEMA_IADH2 STANDARD; PRT; 550 AA P12583; Q84011; O1-CCT-1989 (Rel. 12, Created) O1-APR-1990 (Rel. 14, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Hemagglutinin precursor [Contains: Hemagglutinin HA2 chain] (Fragment).
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin;
NON_TER 1 328 HEMP
Viruses; ssRNA negative-strand Influenza virus A and B group; Influenza A virus.
NCBI_TaxID=11358;
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A27813; HMIV77.
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Influenza A viruses;
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11. FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING CELL RECEPTORS AND FOR INITIATING INFECTION.

11. SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED IN (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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SEQUENCE FROM N.A.
MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W.,
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rPro; IPR001364; Hemagglutn.
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                                                                                             DGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFHQIEKEFSEVEGRIQ
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                                         DLEKYVEDTK------IDLWS-----YNADVLVALEN---QHTIDLT
                                                                   -- EKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFI
                                                                                                                                                    IPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQARGLFGATAGFIENGWEGMI
                                                                                                                                                                             ITSS--YKDYMDTQIPALPKFAKRFSLMV------VQRLLATVAGYVDTPW---Y
                                                                                                                                                                                                           ISIYWTIVKPGDVLVINSNGNLIAPRGYF--KMRTGKSSIMRSDAPIDTCVSECITPNGS
                                                                                                                                                                                                                                     -TLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQH
                                                                                                                                                                                                                                                                  -----W-----GVHHPSTNQEQTNLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGQSRG
                                                                                                                                                                                                                                                                                            TEKRFWMRFRRGKNHSYFHDLVFNLLEKN-----VTRDADATDIENFASRYLYMA----
                                                                                                                                                                                                                                                                                                                        ----ASGFFSRL---NWLTKSGSTYPV----LNVTMPNNDNFDKLYI------
                                                                                                                                                                                                                                                                                                                                                   NCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANS
                                                                                                                                                                                                                                                                                                                                                                             ERSNAFSNCYPY--DVPDYASLRSLVASSGTLKFITEGFTWTGVTQNGGSKACKRGP---
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                                                                                                                          -MKLK------NEMVNRVFIPTKKFFN---KEIREPSKALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. . .) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104;
Pred. No. 8
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ion of H3 influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein.
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Best Local S
Matches 92
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HA1 chain; Hemagglutinin HA2 chain] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 159:109-119(1987).
-i- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=87265458; PubMed=2440178;
Kida H., Kawaoka Y., Naeve C.W., Wel
"Antigenic and genetic conservation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; (Influenza virus A and B group; Influenza Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M16739; AAA43145.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
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SUBUNIT: HOMOTRIMER. EACH OF THE MONDMERS IS FORMED BY TWO
(HA1 AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C27813; HMIV33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                           -----ASGFFSRL---NWLTKSGSTYPV----LNVTMPNNDNFDKLYIWGVHHPSTNQEQ
                                                                                      NCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFI--
                                                                                                                                   ERSNAFSNCYPY -- DVPDYASLRSLVASSGTLEFITEGFTWTGVTQNGGSNACKRGP---
                                                                                                                                                                              ESVDSAANAYMINSDMSDYLS-------AVSDNFAERICSQVPKGS
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--LFKESDANPANSTEK---
                                                                                                                                                                                                                                                      Similarity
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25; Hemagglutn;
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N-LINKED (GLCNAC...) (P
                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                         Score 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEMAGGLUTININ HA1
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                                                                                                                                                                                                                              Mismatches
-- RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
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ion of H3 influenza virus
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a A viruses;
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                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                     Length 550;
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MAP1B OR MTAP1B OR MTAP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Noble M., Lewis S.A., Cowan N.J.; "The microtubule binding domain of MAPIB contains a repeated sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SWISS WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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                                                                                                                                                                                                             SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPIA AND MAPIB PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules. PTM: LC1 IS COEXPRESSED WITH MAPIB IT IS FREE TO ASSOCIATE WITH BOTH MAPIB BY PROTECLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIB AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL BIOL. 109:3367-3376(1989).

FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES

THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAS.

TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNIT

MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                             SIMILARITY: TO MAPIA
                                                                                                                                                                                            BOTH MAP1A
OF MAP1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STABILIZING MICROTUBULES
                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ED process Bioinformatics and the ED process Bioinformatics are the controlled to the controlled by the co
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed

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email to license@isb-sib.ch).
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CARBOHYD
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand Influenza virus A and B group;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M73772; -; NOT_ANNOTATED_CDS HSSP; P03437; 2HMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonhuman hosts.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bean W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92114135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza virus A and Influenza A virus. NCBI_TaxID=11367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hemagglutinin
Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom;
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Viruses; ssRNA negative-strand viruses; Orthomyxo
Influenza virus A and B group; Influenza A viruse
                                                                                                                                                                                                         149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Evolution of the H3 influenza virus hemagglutinin from human
                                               199
                276
                                                                               251
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FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING CELL RECEPTORS AND FOR INITIATING INFECTION.

SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED E (HAL AND HAZ) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                           NFAERICSQVPKGSNCSASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAA 103
                                                                                                                                            YVWGVHHPSTNQEQTDLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGQSGRISIYW---
                                                                                                                                                                          FI-----RFWMRFRRGKNHSYFHDL 138
                                                                                                                                                                                                           NGGSNACKRGP-----ASGFESRL---NWLTKSGSTYPV----LNVTMPNDDNFDKL 193
                                                                                                                                                                                                                                                                      DVFQDETWDLYVERSSAFSNCYPY-----DVPDYASLRSLVASSGTLEFITEGFTWTGVTQ 148
                                                                                                                                                                                                                                                                                                     DSVGDVTKTLLAASESVDSAANAYMINSDMSDYLS------AVSD 43
                IRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQSTLKLATG
                                              IKRALKQIIRSNLPLDIGTEHSVSRLQHITSS--YKDYMDTQIPALPKFAKRFSLMV---
                                                                                                           VFNLLEKNYTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000225;
                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                   Conservative
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HA2 chain].
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Score 103;
Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMAGGLUTININ HA2
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                                                                                                                                                                                                                                                                                                                                     166;
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(POTENTIAL)

188;

Gaps

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RESULT 38

MYSH_ACACA
ID MYSH_AN
AC P47808
DT 01-FEB
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DE High m
OS Acanth
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RN (11)
RP SEQUEN
RN HOTOW!
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RN Pfam;
RN Pfam;
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"A new Acanthamoeba myosin heavy chain. Cloning of th immunological identification of the polypeptide.";

J. Biol. Chem. 265:20646-20652(1990).

-i- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED.
-i- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
High molecular weight form of myosin I (HMWMI).
Acanthamoeba castellanii (Amoeba).
                                                                                                                                                         ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; I.
SMART; SM00242; MYSC; I.
SMART; SM00139; MYTH4; I.
SMART; SM00326; SH3; I.
                                                                                                                           PROSITE; PS50002; SH3; 1
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                     Pfam; PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M60954; AAA27709.1; -. HSSP; P08799; 1MND.
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                                                          DOMAIN
                                                                           DOMAIN
                                                                                                                                                                                                                                                 PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                    Pfam; PF00018;
                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                         DOMAIN
                                                                                                             Myosin;
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                                                                                                                                                                                                                                                                                 PF00063;
PF00784;
                                                                                                         Actin-binding;
                                                                                                                                                                                                                                                                                                                                 IPR000048; IQ.
IPR000857; MyTH4.
IPR001452; SH3.
IPR001609; myosin_
        755
1519
168
628
                                                                                                                                                                                                                                                               SH3;
                                                                                                                                                                                                                                                                                               myosin_head;
                                                                                                                                                                                                                                                                                   MYTH4;
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                                                                                                                                                                                                                                                                                                                                 myosin_head
                                                                                                           ATP-binding;
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IQ.
SH3.
ATP (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
                                                                           MYOSIN
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                                                                                                         Methylation;
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Best Local
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                                                                                                                                                                                                                                          P08096; 074336; 01-AUG-1988 (Rel. 08, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) DNA topoisomerase II (EC 5.99.1.3). TOP2 OR SPBC1A4.03C.
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DOMAIN
DOMAIN
DOMAIN
                                                   SEQUENCE FROM N.A.
MEDLINE-87053875; PubMed-3023070;
Uemura T., Morikawa K., Yanagida M.;
"The nucleotide sequence of the fission yeast
gene: structural and functional relationships
                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
     topoisomerases.";
EMBO J. 5:2355-2361(1986)
[2]
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POLY-GLN.
POLY-GLN.
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SVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSA 65
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LVLDEQISIPKSSDATFFIKANQTQAARSTQLRGGEDSRTDFIIKHYAGDVIYDSTGMLE
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                                                                                                                                                            SKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTV
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STRAIN-972;
Wood V., Ra
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ACT_SITE
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL031174; CAA20107.1;
PIR; A24897; ISZPT2.
HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04326; CAA27857.1; ALT_INIT.
EMBL; AL031174; CAA20107.1; -.
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"A functional 125-kDa core polypeptide
topoisomerase II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003957; CBFA_NFYB_top1s.
InterPro; IPR001941; DNA_top01s0II.
InterPro; IPR002205; DNA_top01s0IV.
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                                                                                                                                                                                                                                                   Nuclear
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SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION MULTIPLE
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NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC EN
RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
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                                      INSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSAYMSRCAK-----QDCLT--LQS 80
                                                                                                                                                                                                                                                                                                       TS; PRO0615; CCAATSUBUNTA.
TS; PRO0418; TPIZFAMILY.
TP SM003616; DNA LOPO150II; 1
T; SM0038; TOP2C; 1.
T; SM00434; TOP4C; 1.
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IDADFSDYEDEASGD--ENVLPNTT--TKRKASTTSSKSRAKKASTPDLRQTSLTSMTAS
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113; Conser
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PS00177; TOPOISOMERASE_II; 1.
PS00177; TOPOISOMERASE_II; 1.
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35 DNA CLEAVAGE (BY SIMILARITY)
94 N -> I (LN REF 1).
167891 MW; 6D88F76243361B2F CRC64;
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                                                                                  62;
                                                                                                 Score 102.5;
Pred. No. 34;
                                                                                  Mismatches
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X-RAY CRYSTALLOGRAPHY
                                         Xu H., Wu X.R., Wewer U.M., Murine muscular dystrophy
                                                                                                                                                   STRAIN=C57BL/6; TISSUE=Thymus; MEDLINE=93346725; PubMed=8345183;
                                                                                                                                                                                                                                            STRAIN-FVB/N; TISSUE-Embryo, and MEDLINE-95316259; PubMed-7795883; Bernier S.M., Utani A., Sugiyama
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                   _MOUSE
                     Nat. Genet.
                                   2 (Lama2)
                                                                               SEQUENCE OF 64-281 FROM N.A.
                                                                                                                                        Chang A.C.,
                                                                                                                                                                          [2]
SEQUENCE OF 2162-2279 FROM N.A.
                                                                                                                                                                                                 Matrix Biol.
                                                                                                                                                                                                           "Cloning and mouse.";
                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                    MEDLINE=95179178;
                                                                                                                                                                                                                                    Yamada Y
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                                                                                                                            Chang A.C., Wadsworth S., Expression of merosin in
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                                                        X.R., Wewer U.M.,
                       8:297-302(1994).
                                                                                                      151:1789-1801(1993).
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ANGSTROMS)
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Sciurognathi; Muridae;
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                                              the
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                                              laminin
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                                              alpha
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AMBL; by Date of the probability of the probability
         MEDLINE-20085745; PubMed-10619025; Hohenester E., Tisi D., Talts J.F., Ti "The crystal structure of a laminin G-molecular basis of alpha-dystroglycan and agrin."; Mol. Cell 4:83-792(1999).
                                                                                                                                                                                             PROSITE; PS000
PROSITE; PS011
PROSITE; PS012
PROSITE; PS500
Glycoprotein;
Laminin EGF-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U12147;
EMBL; X69869;
EMBL; S75315;
PDB; 10U0; 03-
MGD; MGI:9912
    SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE ALPHA-2 CHAIN IS A SUBUN
4 (S-MEROSIN).
1 SUBCELLULAR LOCATION: Extract
1 TISSUE SPECIFICITY: FOUND IN
COMPONENT).
1 DOMAIN: THE ALPHA-HELICAL DOI
WITH OTHER LAMININ CHAINS TO
DOMAIN: DOMAINS VI, IV AND G
DISEASE: DEFECTS IN LAMA2 ARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - SIMILARITY: CONTAINS 1
- SIMILARITY: CONTAINS 1
- SIMILARITY: CONTAINS 2
- SIMILARITY: CONTAINS 2
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SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE ALPHA-2 CHAIN IS A SUBUNIT OF LAMININ-2 (MEROSIN) AND LAMININ-
                                                                                                                                                                                                                                            PS00022;
PS01186;
PS01248;
PS50025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147; AAC52165.1; -.
869; CAA49502.1; -.
315; AAB33573.1; -.
; 03-DEC-99.
                                                                                                                                                                                           1248; LAMININ_TYPE_EGF; 14.
1025; LAM_G_DOMAIN; 5.
18asement membrane; Extrace
11ke domain; Cell adhesion;
       3106
282
339
409
464
513
523
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ture of a laminin G-like module reveals the
alpha-dystroglycan binding to laminins, perlecan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LAMININ N-TERMINAL DOWN
17 LAMININ EGF-LIKE DOMAI
2 LAMININ DOMAINS IV.
5 LAMININ G-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular.
OUND IN THE BASEMENT MEMBRANES
  POTENTIAL.
LAMININ ALL
LAMININ G-
LAMININ EGI
LAMININ EGI
LAMININ EGI
LAMININ EGI
LAMININ EGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAINS I AND II ARE THOUGHT TO INTERACT
TO FORM A COILED COIL STRUCTURE.
D G ARE GLOBULAR.
ARE A CAUSE OF MURINE MUSCULAR DYSTROPHY
                                                                                                                                                                                             Extracellular matrix; Coiled coil;
nesion; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-TERMINAL DOMAIN
EGF-LIKE DOMAINS
N ALPHA-2 CHAIN.

N N-TERMINAL (DOMAIN VI).

N EGF-LIKE 1.

N EGF-LIKE 3.

N EGF-LIKE 4.

N EGF-LIKE 5 (N-TERMINAL).
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N EGF-LIKE 7.
N EGF-LIKE 7.
N EGF-LIKE 1.
N EGF-LIKE 11.
N EGF-LIKE
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5 (C-TERMINAL).
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(C-TERMINAL).
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